

MEETING AGENDA

Thursday, September 14

14:30-14:45 **WELCOME**

Session 1 Structural Variation
Moderator- Stephen Chanock

14:45-15:10 **Stephen Scherer**

Discovery of Structural Variation in the Human Genome: New Insights for Disease Study

15:10-15:25 **Alexander Urban**

High-Resolution Mapping of DNA Copy-Number Alterations Using High-Density Tiling Oligonucleotide Arrays

15:25-15:50 **Anthony Brookes**

Hidden' Copy-Number Variation: A Technically Challenging and Seemingly Common Feature of the Human Genome

15:50-16:05 **Charles Lee**

Hotspots for Copy Number Variation in Chimpanzees and Humans

16:05-16:30 **Evan Eichler**

Sequence-Based Resolution of Human Genome Structural Variation

16:30-18:30 **POSTER SESSION #1**

Session 2 Technology
Moderator- Anthony Brookes

18:30-18:55 **Kenshi Hayashi**

D-Haplo: A Genome-Wide Definitive Haplotypes Determined using Complete Hydatidiform Moles

18:55-19:10 **David Bentley**

Using Next Generation Technology for Human Genome Sequencing and SNP Discovery

19:10-19:35 **Jingyue Ju**

Four-Color DNA Sequencing by Synthesis Using Cleavable Fluorescent Nucleotide Reversible Terminators

19:35-20:00 **Elaine Mardis**

Impact and Integration of New Genomics Technologies

20:00-22:00 **DINNER (Prompt Restaurant)**

Friday, September 15

Session 3 Variation and Expression ***Moderator- Stephen Scherer***

8:00-8:25 Vivian Nap-Yee Chan

Genomic Variations in Disease by Allele-Specific Arrayed Primer Extension (AS-APEX)
Microarray Detection System

8:25-8:50 Daniel Schaid

Scanning for "Hot Spot" SNPs Having a Large Number of Trans-Effects on Quantitative
Gene Expressions

8:50-9:15 Edison Liu

Comprehensive and Precise Mapping of p53 Effects

9:15-9:30 Andrew Dunham

Exon Resequencing: The Search for Sequence Variation in Human Genome

Keynote Lecture (Introduction by Carlos Bustamante)

9:30-10:05 Andrew Clark

The Era of Cheap Genome-Wide SNPs

10:05-10:30 BREAK

Session 4 Patterns of Variation ***Moderator- Carlos Bustamante***

10:30-10:55 Molly Przeworski

The Evolution of Mendelian Disease Genes

10:55-11:20 Nathan Sutter

An Ancient Haplotype Identical In 17 Toy Dog Breeds Pinpoints A Major Gene For
Body Size

11:20-11:45 Pui-Yan Kwok

Technological Approaches to Genome-Wide and Candidate Gene Association Studies

11:45-12:10 Jonathan Pritchard

A Worldwide Survey of Haplotype Variation and Linkage Disequilibrium in the
Human Genome

12:10-12:35 Neil Risch

Whole Genome Association Studies in Admixed Populations

12:40-14:00

LUNCH (Prompt Restaurant)

Session 5 Whole Genome Scans

Moderator- Charles Rotimi

14:00-14:25 Goncalo Abecasis

Efficient Design and Analysis of Genome Wide Association Studies

14:25-14:40 Christoph Lange

Screening and Testing Using the Same Data Set: A Testing Strategy for Genome-Wide Association Studies for Case/Control Designs

14:40-14:55 Pak-Chung Sham

Estimation of Global and Local Genomic Sharing using Genome-Wide SNP Data

14:55-15:20 Stephen Chanock

Whole Genome Scans in Breast and Prostate Cancer: Cancer Genetic Markers of Susceptibility (CGEMS)

15:20-15:35 Hidetoshi Inoko

Genome-wide Scan of Disease Genes by Association Analysis Using 30,000 Microsatellites

15:35-17:30

POSTER SESSION #2

Session 6 Variation & Disease

Moderator- Paul Kwong-Hang Tam

17:30-17:55 Charles Rotimi

Understanding the Genetic Basis of Type 2 Diabetes in Populations of the African Diaspora

17:55-18:10 Grant Montgomery

Novel Variants in GDF9 in Mothers of Dizygotic Twins

18:10-18:25 Francisco De la Vega

A Genome-Wide Direct Association Study of Crohn's Disease with 19,772 Putative Functional Coding SNPs.

18:25-18:50 Kyuyoung Song

Association of CD30 with Systemic Lupus Erythematosus in Korean, Japanese, and Chinese Populations

19:00-21:00

DINNER (La Dynastie Restaurant)

Saturday, September 16

Session 7 Molecular Evolution ***Moderator- Andrew Clark***

8:30-8:55 **Li Jin**
TBA

8:55-9:20 **Rasmus Nielsen**
Darwinian and Demographic Forces Affecting Human Genes

9:20-9:45 **Peter Keightley**
Nature of Selective Constraints on Non-coding DNA of Mammals

9:45-10:00 **Constantin Polychronakos**
Strand Bias in Complementary Single-Nucleotide Polymorphisms: Evidence for Functional Effects of Synonymous Substitutions

10:00-10:25 **Carlos Bustamante**
Robust Inference of Natural Selection on the Human Genome

10:25-11:00 **BREAK**

Session 8 Variation and Outcome ***Moderator- Pui-Yan Kwok***

11:00-11:25 **Paul Kwong-Hang Tam**
Approaches to the Genetic Analysis of an Oligogenic Disease: Hirschsprung's Disease

11:25-11:50 **Yuan-Tsong Chen**
Genetic Susceptibility to Severe Adverse Drug Reactions: Perspective for Future Medicine

11:50-12:05 **Chack-Yung Yu**
Gene Copy Number Variation in Human Autoimmune Disease Systemic Lupus Erythematosus (SLE)

12:05-12:30 **Magnus Ingelman-Sundberg**
Copy-Number Variation in Cytochrome P450 Genes and Differential Drug Responses

12:30-13:00 **CLOSING DISCUSSION**

13:00-14:30 **LUNCH (La Dynastie Restaurant)**

14:45-21:00 **EXCURSION & BANQUET**